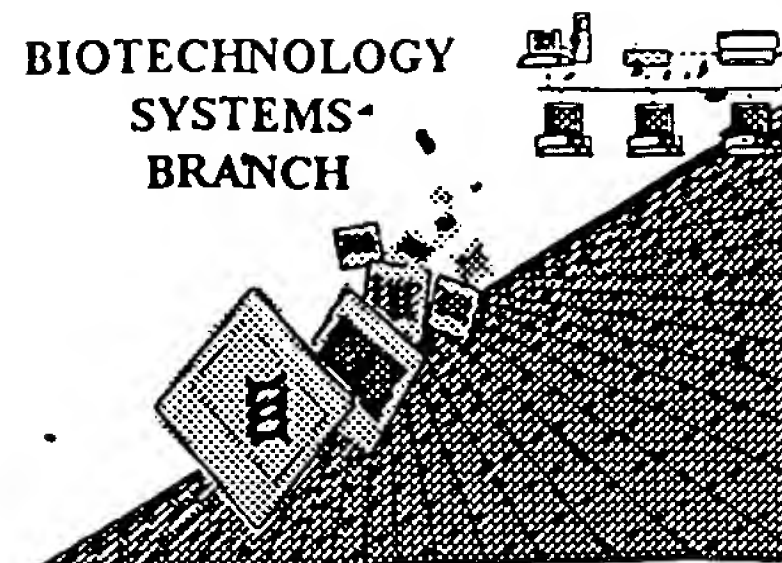


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/357522
Source: PCT09
Date Processed by STIC: 11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/857522

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 Patentln 2.0
 "bug"
A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 Patentln 2.0
 "bug"
Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,522

DATE: 11/14/2001

TIME: 14:03:49

Input Set : A:\BB1315 PCT Seq List.txt

Output Set: N:\CRF3\11142001\I857522.raw

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
 4 Pioneer Hi-Bred International, Inc.
 6 <120> TITLE OF INVENTION: Plant Carbon Catabolite Repression Proteins
 8 <130> FILE REFERENCE: BB1315
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/857,522
 C--> 11 <141> CURRENT FILING DATE: 2001-11-14
 13 <150> PRIOR APPLICATION NUMBER: 60/112,563
 14 <151> PRIOR FILING DATE: 1998-12-16
 16 <160> NUMBER OF SEQ ID NOS: 28
 18 <170> SOFTWARE: Microsoft Office 97

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

1595 <210> SEQ ID NO: 28
 1596 <211> LENGTH: 85
 1597 <212> TYPE: PRT
 1598 <213> ORGANISM: Triticum aestivum
 1600 <220> FEATURE:
 1601 <221> NAME/KEY: UNSURE
 1602 <222> LOCATION: (29)
 1604 <220> FEATURE:
 1605 <221> NAME/KEY: UNSURE
 1606 <222> LOCATION: (48)
 1608 <220> FEATURE:
 1609 <221> NAME/KEY: UNSURE
 1610 <222> LOCATION: (50)
 1612 <220> FEATURE:
 1613 <221> NAME/KEY: UNSURE
 1614 <222> LOCATION: (69)
 1616 <220> FEATURE:
 1617 <221> NAME/KEY: UNSURE
 1618 <222> LOCATION: (75)
 1620 <220> FEATURE:
 1621 <221> NAME/KEY: UNSURE
 1622 <222> LOCATION: (80)
 1624 <220> FEATURE:
 1625 <221> NAME/KEY: UNSURE
 1626 <222> LOCATION: (82)
 1628 <400> SEQUENCE: 28
 1629 Leu Lys Asn Tyr Arg Ile Gly Lys Thr Leu Gly Ile Gly Ser Phe Gly
 1630 1 5 10 15
 W--> 1632 Lys Val Lys Ile Ala Glu His Ile Lys Thr Gly His Xaa Val Ala Val
 1633 20 25 30
 W--> 1635 Lys Ile Leu Asn Arg Arg Gln Ile Lys Asn Met Ala Met Glu Glu Xaa
 1636 35 40 45
 W--> 1638 Val Xaa Arg Glu Ile Lys Ile Leu Arg Leu Phe Met His Pro His Ile

*Errored - must enumerate in
 field 223 which ~~PROTEIN~~ amino
 acids are your intended protein values*

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,522

DATE: 11/14/2001

TIME: 14:03:50

Input Set : A:\BB1315 PCT Seq List.txt

Output Set: N:\CRF3\11142001\I857522.raw

```
      1639      50      55      60
W--> 1641 Ile Arg Leu Tyr Xaa Val Ile Glu Ala Pro Xaa Asp Ile Tyr Val Xaa
      1642 65      70      75      80
W--> 1644 Met Xaa Tyr Val Lys
      1645      85
E--> 1647 28
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/857,522

DATE: 11/14/2001

TIME: 14:03:51

Input Set : A:\BB1315 PCT Seq List.txt

Output Set: N:\CRF3\11142001\I857522.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:482 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:483 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1495 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1589 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1590 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1591 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1592 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1593 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1632 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1638 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1641 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1644 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:1644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1647 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28